AMENDMENTS TO THE CLAIMS

Please amend claims 1, 3, 8, 9, 13, 25, and 36 as set forth below. Claims 2, 10, 11, 14-22, 24, 27-35, 37, 39-47, and 49-79 were previously canceled.

The current listing of claims replaces all prior listings.

1. (Currently Amended) A method for determining the gender of a subject from the canis familiaris species, comprising:

a) contacting a nucleic acid sample from the subject with a first and a second oligonucleotide ~~probe or~~ primer, wherein the first and/or second oligonucleotide ~~probe or~~ primer is complementary to consensus regions between SEQ ID NO:22 and SEQ ID NO:23, and wherein such first and second ~~probes or~~ primers flank non-consensus regions between SEQ ID NO:22 and SEQ ID NO:23;

b) amplifying the flanked non-consensus regions, wherein the flanked non-consensus regions of SEQ ID NO:22 contain at least one gap in sequence alignment compared to the flanked non-consensus regions of SEQ ID NO:23, such that different length amplification products result if sequences comprising both SEQ ID NO:22 and SEQ ID NO:23 are present in the sample ~~binding the first and second oligonucleotide probes or primers to the sample nucleic acid under conditions sufficient for hybridization of the probes or primers to the sample nucleic acid~~; and

c) detecting ~~non-consensus regions which are specific to SEQ ID NO: 22 and/or specific to SEQ ID NO:23 in~~ amplification products resulting from ~~the binding of~~ step (b), wherein detection of ~~non-consensus regions which are specific to SEQ ID NO:22 and SEQ ID NO:23~~ amplification products of different lengths correlates with male gender ~~the presence of X and Y chromosomal DNA of the species in the nucleic acid sample~~.

2. (Canceled)

3. (Currently Amended) The method of claim 1, ~~further~~ comprising determining the presence of amplified products as set forth in SEQ ID NO: 10 and SEQ ID NO:11.

4. (Previously Presented) The method of claim 3, wherein the first oligonucleotide primer binds to SEQ ID NO:6 and SEQ ID NO:7 and the second oligonucleotide primer binds to SEQ ID NO:8 and SEQ ID NO:9.

5. (Original) The method of claim 4, wherein the first primer comprises at least 10 nucleotides of SEQ ID NO:3 and the second primer comprises at least 10 nucleotides of SEQ ID NO:5.

6. (Original) The method of claim 5, wherein the first primer is SEQ ID NO:3 and the second primer is SEQ ID NO:5.

7. (Original) The method of claim 5, wherein the first primer is SEQ ID NO:4 and the second primer is SEQ ID NO:5.

8. (Currently Amended) The method of claim 5, ~~wherein the oligonucleotide primers generate amplification products that are of different lengths,~~ wherein a first length is indicative of ~~a~~ the non-consensus region of ~~specific to~~ SEQ ID NO:22 ~~which correlates with an X chromosome of the species~~ and a second length is indicative of ~~a~~ the non-consensus region of ~~specific to~~ SEQ ID NO:23 ~~which correlates with a Y chromosome of the species~~.

9. (Currently Amended) A method for determining the gender of a subject from the canis familiaris species, comprising:

a) contacting a nucleic acid sample from the subject with a first and a second oligonucleotide ~~probe or~~ primer, wherein the first and second oligonucleotide ~~probes or~~ primers comprise sequences which are complementary to ~~non-~~consensus regions between SEQ ID NO:22

and SEQ ID NO:23, and wherein such first and second primers flank non-consensus regions between SEQ ID NO22 and SEQ ID NO:23;

b) amplifying the non-consensus regions, wherein the non-consensus regions of SEQ ID NO:22 contain at least one gap in sequence alignment compared to the non-consensus regions of SEQ ID NO:23, such that a single product results if non-consensus sequences of SEQ ID NO:23 are absent in the sample; and

c) ~~detecting~~ determining the presence or absence of the non-consensus regions ~~which are specific to SEQ ID NO:22 and/or specific to SEQ ID NO:23~~ in products resulting from the ~~binding~~ amplification ~~of~~ in step (b),

wherein failure to ~~detect~~ determine the non-consensus regions comprising ~~which are specific to~~ SEQ ID NO: 23 correlates with female gender ~~is indicative of the absence of Y chromosomal DNA of the species in the nucleic acid sample~~.

Claims 10-11. (Canceled)

12. (Previously Presented) The method of claim 9, wherein a first oligonucleotide primer binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second oligonucleotide primer binds to SEQ ID NO:8 and/or SEQ ID NO:9.

13. (Currently Amended) The method of claim 9, wherein amplification of ~~binding of the first and second oligonucleotide probes or primers to~~ non-consensus regions of ~~specific to~~ SEQ ID NO:22 or ~~specific to~~ SEQ ID NO:23 distinguish ~~an amelogenin gene~~ the male gender of the species ~~on an X chromosome~~ from ~~an amelogenin gene~~ the female gender of the species ~~on the Y chromosome in the sample~~.

Claims 14-22. (Canceled)

23. (Previously Presented) A method of detecting binding of at least two oligonucleotide primers to a canine amelogenin gene, wherein the at least two oligonucleotide primers are complementary to a sequence of SEQ ID NO:22 and/or SEQ ID NO:23, comprising:

a) contacting a nucleic acid sample from a canine subject with the at least two oligonucleotide primers, wherein the complementary regions flank non-consensus regions between SEQ ID NO:22 and SEQ ID NO:23;

b) binding the at least two oligonucleotide primers to the sample nucleic acid under conditions sufficient for hybridization of the oligonucleotide primers to the sample nucleic acid; and

c) detecting binding between the at least two oligonucleotide primers and the sample nucleic acid,

wherein detection of binding is indicative of the presence of homologous canine amelogenin sequences in the sample.

24. (Canceled)

25. (Currently Amended) The method of claim 23, wherein the at least two primers generates an amplification product as set forth in SEQ ID NO:10 or SEQ ID NO:11.

26. (Previously Presented) The method of claim 25, wherein a first primer of the at least two oligonucleotide primers is complementary to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer is complementary to SEQ ID NO:8 and/or SEQ ID NO:9.

Claims 27-35. (Canceled)

36. (Currently Amended) A method of genotyping a canis familiaris subject, comprising:

a) contacting a nucleic acid sample from the canis familiaris subject with at least two sets of ~~probes or~~ primers, wherein the first set of probes or primers comprises first and second oligonucleotide ~~probes or~~ primers which are complementary to consensus regions between SEQ

ID NO:22 and SEQ ID NO:23 and flank non-consensus regions between SEQ ID NO:22 and SEQ ID NO:23, and wherein the second set of ~~probes or~~ primers comprises third and fourth oligonucleotide ~~probes or~~ primers which are complementary to at least one microsatellite locus;

b) amplifying the flanked non-consensus regions, wherein the flanked non-consensus regions of SEQ ID NO:22 contain at least one gap in sequence alignment compared to the flanked non-consensus regions of SEQ ID NO:23, such that different length amplification products result if sequences comprising both SEQ ID NO:22 and SEQ ID NO:23 are present in the sample;

c) amplifying the microsatellite locus;

~~binding the probes or primers to the sample nucleic acid under conditions sufficient for hybridization of the probes or primers to the sample nucleic acid~~; and

d) detecting ~~differences in~~ different amplified products ~~resulting from the binding of the probes or primers~~, wherein the different products correlate with a particular genotype presented by the canis familiaris subject.

37. (Canceled)

38. (Previously Presented) The method of claim 36, wherein the first and second primers generate amplification products as set forth in SEQ ID NO:10 and SEQ ID NO:11.

Claims 39-47. (Canceled)

48. (Previously Presented) The method of claim 36, wherein the microsatellite locus is at least one of PEZ1/CATA1, PEZ3, PEZ5, PEZ6, PEZ8, PEZ10, PEZ11, PEZ12, PEZ13, PEZ15, PEZ16, PEZ17, PEZ20, PEZ21, FH2010, FH2054, and FH2079.

Claims 49-79. (Canceled)

80. (Previously Presented) The method of any of claims 12, 25 or 38, wherein the first primer is SEQ ID NO:4 and the second primer is SEQ ID NO:5.

81. (Previously Presented) The method of any of claims 12, 25 or 38, wherein the first primer is SEQ ID NO:3 and the second primer is SEQ ID NO:5.